#4

N-TERMINAL AMINOACID SEQUENCES

Position	A	B	C
01			LEU
02			ALA
03			VAL
04			PRO
05		ALA	ALA
06		SER	SER
07		---	ARG
08	---**	---	ASN
09	GLN	GLN	GLN
10	SER	SER	SER
11	SER	SER	SER
12	---	---	GLY
13	ASP	ASP	ASP
14	THR	THR	THR
15	VAL	VAL	VAL
16	ASP	ASP	ASP
17	GLN	GLN	
18		GLY	
19		TYR	
20		GLN	
21		ARG	
22		PHE	
23		SER	
24		GLU	
25		THR	
26		SER	
27		HIS	
28		LEU	
29		ARG	
30		(GLY)*	
31		GLN	
32		TYR	
33		ALA	
34		PRO	
35		PHE	
36		PHE	
37		(ASP)	
38		LEU	
39		ALA	

FIG. 1 A

PEPTIDE AMINOACID SEQUENCES

Position	A	B	C	D	E
01	GLN	(TRP)*	MET	ALA	VAL
02	———**	SER	MET	SER	VAL
03	GLN	PHE	GLN	SER	ASP
04	ALA	ASP	CYS	ALA	———
05	GLU	THR	GLN	GLU	ARG
06	GLN	ILE	ALA	LYS	PHE
07	GLU	SER	GLU	GLY	PRO
08	PRO	THR	GLN	TYR	TYR
09	LEU	SER	GLU	ASP	THR
10	VAL	THR	PRO	LEU	GLY
11	(ARG)	VAL	LEU	VAL	———
12	VAL	ASP	VAL	VAL	ALA
13	LEU	THR	ARG		
14	VAL	LYS	VAL		
15	ASN	LEU	LEU		
16	(ASP)	SER	VAL		
17	(ARG)	PRO	ASN		
18	(VAL)	PHE	ASP		
19	VAL	(CYS)	ARG		
20	PRO	(ASP)			
21		LEU			
22		PHE			
23		THR			

FIG. 1B

N-TERMINUS 100KD PROTEIN

Position	
01	VAL
02	VAL
03	ASP
04	GLU
05	ARG
06	PHE
07	PRO
08	TYR
09	THR
10	GLY

FIG. 1C

```
             1   2   3   4   5   6   7   8   9   10  11  12  13  14  15  16  17  18  19  20
Peptide C:   Leu-Ala-Val-Pro-Ala-Ser-Arg-Asn-Gln-Ser-Ser-Gly-Asp-Thr-Val-Asp
Peptide B:                   Ala-Ser-***-***-Gln-Ser-Ser-***-Asp-Thr-Val Asp-Gln-Gly-Tyr-Gln-
Peptide A:                                   ***-Gln-Ser-Ser-***-Asp-Thr-Val-Asp-Gln

Possible
codons:5'    CTG-GCG-GTG-CCG-GCG-TCG-CGG-AAT-CAA-TCG-TCG-GGG-GAT-ACG-GTG-GAT-CAA-GGG-TAT- CAA-
               A   A   A   A   A   A   A   C   G   A   A   A   C   A   A   C   G   A   C   G
               T   T   T   T   T   T   T           T   T   T       T   T           T
               C   C   C   C   C   C   C           C   C   C       C   C           C
             TTA                     AGT AGA         AGT AGT
               G                       C   G           C   C

AB1024:        3'-CGG-CAG-GGG-CGG-TCG-GCG-TTG-GTC-TCG-TCG-CCG-CTG-TGG-CAG-CTG-GTC
AB1065:                                                 3'-CCG-CTG-TGG-CAC-CTG-GTC
                                                                           A
AB1066:                                                                G
AB1067:                                                            A
AB1068:                                                        A
AB1069:                                                    A
AB1070:                                                    A   A   A   G   A
AB1226:                                                            3'-CAG-CTG-GTC-CCG-ATG-GTC
                                                                       C   A       A
AB1227:                                                            3'-CAG-CTG-GTC-CCG-ATG-GTC
                                                                       C   A   T   A   A   T
                                                                       A           T

AB1298:                                                    3'-CTG-TGG-CAG-CTG-GTG-CCG-ATG-GTC
                                                               A   C   C   A   T   C   A   T
```

FIG.2A-1

(phytase N-terminus, continued)

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39
Peptide B:	(Arg)	Phe	Ser	Glu	Thr	Ser	His	Leu	Arg	(Gly)	Gln	Tyr	Ala	Pro	Phe	Phe	(Asp)	Leu	Ala
	CGG-	TTT-	TCG-	GAG-	ACG-	TCG-	CAT-	CTG-	CGG-	GGG-	CAG-	TAT-	CGC-	CCG-	TTT-	TTT-	GAT-	CTG-	GCG
	T	A	C	A	A	A	A	C	A	A	A	C	C	A	C	C	C	A	A
	T		T		T	T		T	T	T			T	T				T	T
	C		C		C	C		C	C	C			C	C				C	C
	AGG		AGT			AGT		TTG	AGG									TTG	
	A		C			C		A	A									A	

AB1388:

3'-	CCG-	GTC-	ATG-	CGG-	GGG-	AAG-	AAG-	CTG-	GA
	C				C	C												A	

FIG.2A-2

```
          1  2  3  4  5  6  7  8  9  10 11       12 13 14 15
Peptide A: (Gln- ? -Gln-Ala-Glu-Gln-Glu-Pro-Leu-Val-(Ser/Arg)-Val-Leu-Val-(Asp/Asn)

          CAG-???-CAG-GCG-GAG-CAG-GAG-CCG-CTG-GTG-(TCG/CGG)-GTG-CTG-GTG-(GAT/AAT)
            A      A  A  A  A  A  A  A  A  A  A  A  A  A  A  C  C
                           T              T  T  T  T  T  T  T  T
                           C              C  C  C  C  C  C  C  C
                                       TTG    AGT AGG    TTG
                                          A      C          A

AB1295:          3'-GTC.CGC.CTC.GTC.CTC.GGG.GAG.CA-5'
                      T  G  T  T  T  C A C

          16          17       18 19  20  21  22
          -Asp/Thr/Arg-(Arg/Val)-Val-Pro-(Pro)-Met-Gly

          -GAT/ACG/CGG-(CGG/GTG)-GTG-CCG-(CCG)-ATG-GGG
          C  A  A  A  A  A  A  A     A
                T  T  T  T  T  T     T
                C  C  C  C  C  C     C
             AGG AGG
               A  A
```

FIG.2B-1

```
                1   2   3   4   5   6   7   8   9   10  11  12  13  14  15  16  17  18
Peptide B:  (Trp)-Ser-Phe-Asp-Thr-Ile-Ser-Thr- Ser-Thr-Val-Asp-Thr-Lys-Leu-Ser-Pro-Phe-

            (TGG)-TCG-TTT-GAT-ACG-ATA-TCG-ACG-TCG-ACG-GTG-GAT-ACG-AAG-CTG-TCG-CCG-TTT-
                  A   C   C   A   T   A   A   A   A   A   C   A   A   A   A   A   C
                  T           T   C   T   T   T   T   T       T       T   T   T
                  C           C       C   C   C   C   C       C       C   C   C
                AGT                   AGT     AGT                       TTG AGT
                  C                   C       C                           A   C

AB1296 :          3'-AAG. CTG. TGC. TAG. AGG. TGG. AGG. TGG. CAC.  CTG. TGC. TTC-5'
                                       TCC     C TCC     C

AB1297:  3'-GGC.AAG.
               G

                19  20  21  22  23  24  25  26  27  28  29      30  31      32  33
(Cys)-(Asp)-Leu-Phe-Thr-(Thr)-(Asp)-(Glu)-(Cys)-(Ile)-(Thr/Asn)-(Tyr)-(Arg/Gly)-(Tyr)-Leu

(GTG)-(GAT)- CTG- TTT- ACG-(ACG)-(GAT)- GAG) - (TGT)-(ATA)-(ACG/AAT) - (TAT)-(CGG/GGG)-(TAT)-CTG
  C   C     A   C   A   A   C   A   C   T   A   C   C   A   A   C   A
            T       T   T                   C   T       T   T       T
            C       C   C                       C       C   C       C
          TTG                                             AGG       TTG
            A                                               A         A

(ACG). (CTG). GAG.  AAG. TGC. (TGC). (CTG). (CTC).  (ACG).(TAG). (T)-5'
               C        G   G
```

FIG.2B-2

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23

Phe-Ser-Tyr-Gly-Ala-Ala-Ile-Pro-Gln-Ser-Thr-Gln-Glu-Lys-Gln-Phe-Ser-Gln-Glu-Phe-Arg-Asp-Gly

```
5'-TTT-TCG-TAT-GGG-GCG-GCG ATA-CCG-CAG-TCG-ACG-CAG-GAG-AAG-CAG-TTT-TCG-CAG-GAG-TTT-CGG-GAT- GGG
     C   A   C   A   A   A   T   A   A   A   A   A   A   A   A   C   A   A   A   C   A   C   A
         T       T   T   T   C   T       T   T                       T               T       T
         C       C   C   C       C       C   C                       C               C       C
       AGT                             AGT                         AGT             AGG
         C                               C                           C               C
```

```
AB1025: 3'-ATG-CCG-CGG-CGG-TAG-GGG-GTC-TCG-TGG-GTC-CTC-TTC-GTC-AAG-TCG-GTC-CTC-AAG-GC-5
AB1026:                                     3'-GTC-CTC-TTC-GTC-AAG-TCG-GTC-CTC-AAG-GC-5
                                                     T             AGA       T
                                                                     C

AB1027: 3'-ATG-CCG-GCG-CGC-TAA-GGC-GTC-5'
                 A   T   T   G   G
                     A   A
                     G   G
```

FIG.3

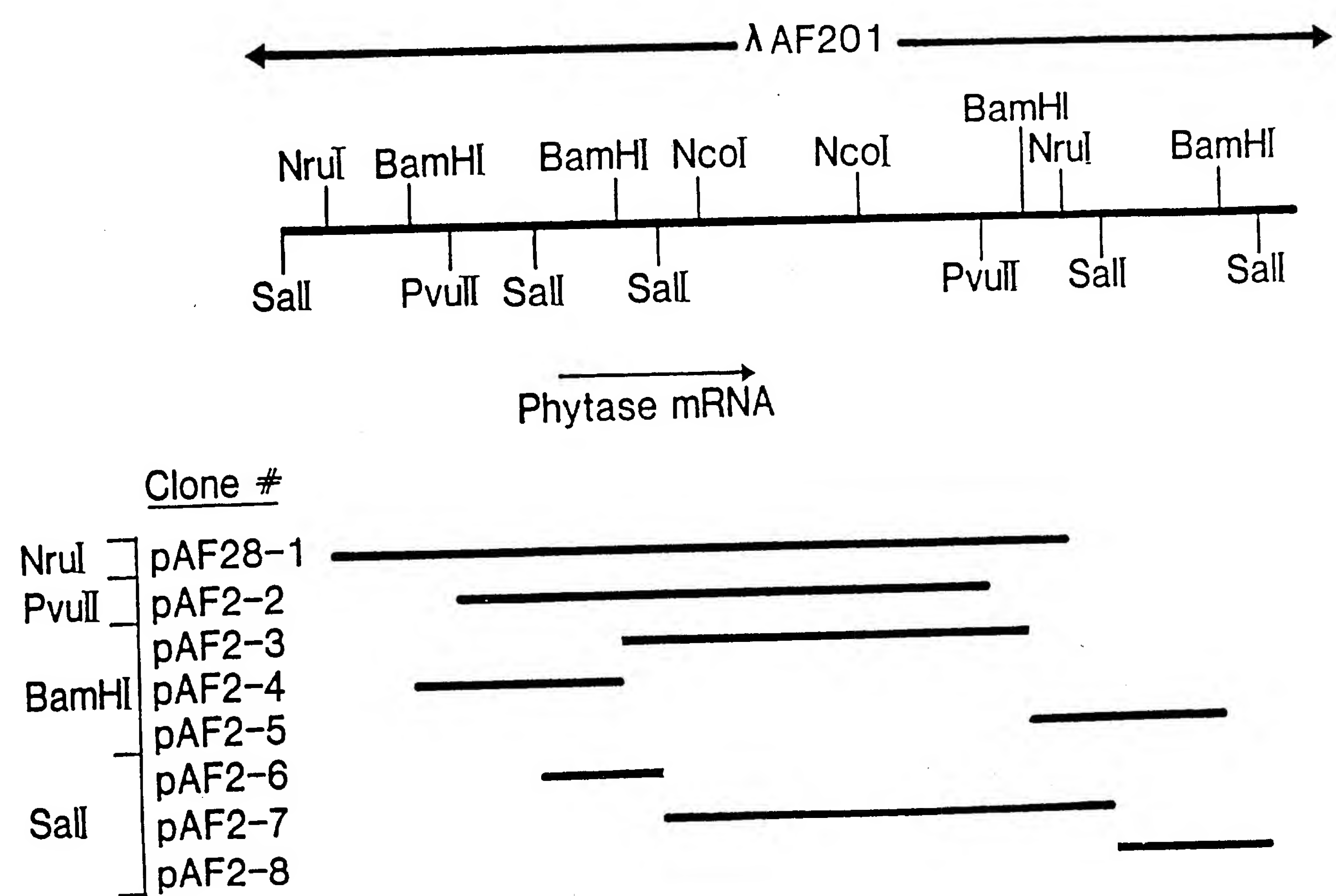

FIG.4

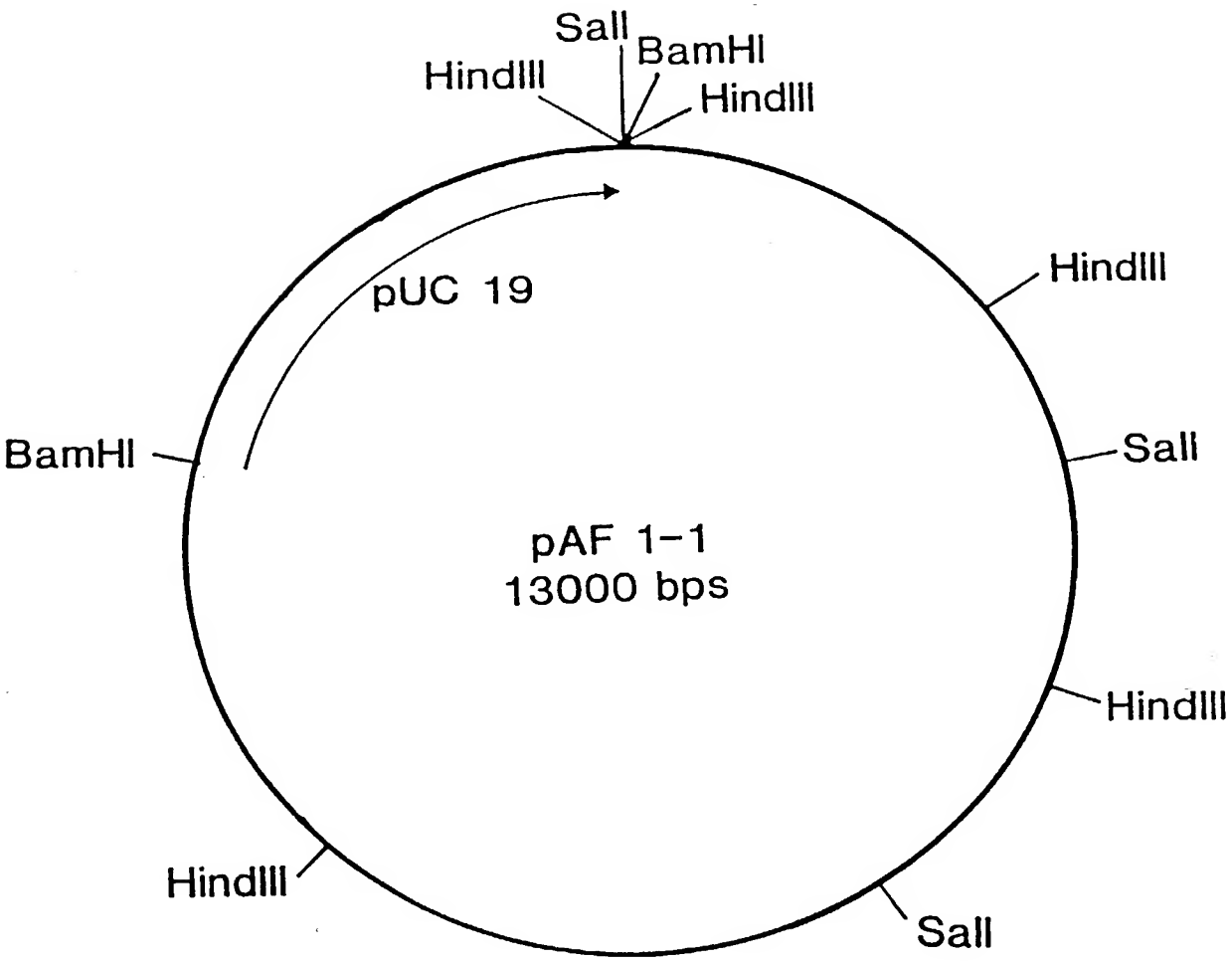

FIG.5

```
GTCGACTTCCCGTCCTATTCGGCCTCGTCCGCTGAAGATCCATCCCACCA
 SalI

TTGCACGTGGGCCACCTTTGTGAGCTTCTAACCTGAACTGGTAGAGTATC    100

ACACACCATGCCAAGGTGGGATGAAGGGGTTATATGAGACCGTCCGGTCC

GGCGCGATGGCCGTAGCTGCCACTCGCTGCTGTGCAAGAAATTACTTCTC    200

ATAGGCATCATGGGCGTCTCTGCTGTTCTACTTCCTTTGTATCTCCTGTC
          translation start

TGGGTATGCTAAGCACCACAATCAAAGTCTAATAAGGACCCTCCCTTCCG    300
   start<----------------------------------------

AGGGCCCCTGAAGCTCGGACTGTGTGGGACTACTGATCGCTGACTATCTG
--intron----------------------------------------

TGCAGAGTCACCTCCGGACTGGCAGTCCCCGCCTCGAGAAATCAATCCAG    400
->end

TTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATC

TTTGGGGTCAATACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCATC    500

TCCCCTGAGGTGCCCGCCGGATGCAGAGTCACTTTCGCTCAGGTCCTCTC

CCGTCATGGAGCGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCG    600

CTCTCATTGAGGAGATCCAGCAGAACGCGACCACCTTTGACGGAAAATAT

GCCTTCCTGAAGACATACAACTACAGCTTGGGTGCAGATGACCTGACTCC    700

CTTCGGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAGCGGT

ACGAATCGCTCACAAGGAACATCGTTCCATTCATCCGATCCTCTGGCTCC    800

AGCCGCGTGATCGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCAC

CAAGCTGAAGGATCCTCGTGCCCAGCCCGGCCAATCGTCGCCCAAGATCG    900
          BamHI

ACGTGGTCATTTCCGAGGCCAGCTCATCCAACAACACTCTCGACCCAGGC

ACCTGCACTGTCTTCGAAGACAGCGAATTGGCCGATACCGTCGAAGCCAA   1000
```

FIG.6A

```
TTTCACCGCCACGTTCGTCCCCTCCATTCGTCAACGTCTGGAGAACGACC

TGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTACCTCATGGACATG   1100

TGCTCCTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTGTCCCC
                               SalI

CTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCC   1200

AGTCCTTGAAAAAGTATTACGGCCATGGTGCAGGTAACCCGCTCGGCCCG

ACCCAGGGCGTCGGCTACGCTAACGAGCTCATCGCCCGTCTGACCCACTC   1300

GCCTGTCCACGATGACACCAGTTCCAACCACACTTTGGACTCGAGCCCGG

CTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTTTCGCATGACAAC   1400

GGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAGCC

GCTATCTACCACGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGT   1500

CTGCTTGGACGGTTCCGTTTGCTTCGCGTTTGTACGTCGAGATGATGCAG

TGTCAGGCGGAGCAGGAGCCGCTGGTCCGTGTCTTGGTTAATGATCGCGT   1600

TGTCCCGCTGCATGGGTGTCCGGTTGATGCTTTGGGGAGATGTACCCGGG

ATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCG   1700

GAGTGTTTTGCTTAGCTGAATTACCTTGATGAATGGTATGTATCACATTG
translation stop

CATATCATTAGCACTTCAGGTATGTATTATCGAAGATGTATATCGAAAGG   1800

ATCAATGGTGACTGTCACTGGTTATCTGAATATCCCTCTATACCTCGTCC

CACAACCAATCATCACCCTTTAAACAATCACACTCAACGCACAGCGTACA   1900

AACGAACAAACGCACAAAGAATATTTTACACTCCTCCCCAACGCAATACC

AACCGCAATTCATCATACCTCATATAAATACAATACAATACAATACATCC   2000
```

FIG.6B

ATCCCTACCCTCAAGTCCACCCATCCTATAATCAATCCCTACTTACTTAC

TTCTCCCCCTCCCCCTCACCCTTCCCAGAACTCACCCCCGAAGTAGTAAT 2100

AGTAGTAGTAGAAGAAGCAGACGACCTCTCCACCAATCTCTTCGGCCTCT

TATCCCCATACGCTACACAAAACCCCCACCCCGTTAGCATGCACTCAGAA 2200

AATAATCAAAAATAACTAAGAAGGAAAAAAAAGAAGAAGAAAGGTTACAT

ACTCCTCTCATACAAACTCCAAGACGTATACATCAAGATGGGCAATCCCA 2300

CCATTACTGATATCCATCTATGAACCCATTCCCATCCCACGTTAGTTGAT

TACTTTACTTAGAAGAAGAAAAAGGGAAGGGAAGGGAAAGAAGTGGATGG 2400

GATTGAGTTAGTGCTCACCGTCTCGCAGCAAGTTTATATTCTTTTGTTTG

GCGGATATCTTTCACTGCTCCTGCTGGACGTTGTCACGGGGTGGTAGTGG 2500

TTGGCGGTGGTGAGGGTCCATGATCACTCTTGGTTTGGGGGGTTGTTGTT

GTCGTTGTTGTTGTTGTTGGGTGGGCATTTTCTTTTCTTCACTTGGGGAT 2600

TATTATTTGGAATTGGTTAGTTTGAGTGAGTGGGTAATATTGAATGGGTG

ATTATTGGGAATGAAGTAGATTTGGCTATGAATGGTTGATGGGATGGAAT 2700

GAATGGATGGATGAATAGATGGAGGCGGAAAAGTCAGGTGGTTTGAGGTT

CGGATTATTATCTTTGTGCCTGAGGCATCACTCTCCATCTATGTTGTTCT 2800

TTCTATACCGATCTACCAGAGCTAAGTTGACTGATTCTACCACAGTGCAC

AATAAGTATGTACTTATTTCATTTAGAGTATTTAGATTAACCCGCTGTGC 2900

TATTTGCCGTAGCTTTCCACCCAATTTCGAAGTTCGAAGAATTAAAACTC

ATCCTACAGTACAGAATAGAAGTAAAAGGAGAAGAGAAAAACAAGATAAT 3000

FIG.6C

ACAACCAGTCCAGGTCCATTCTAGATCTCGAATGACCACCAAATAAGAAA

GCAACAAGCAAGTAAGCAAAGCATAAGTCTAAATGAACGCCAATAACTTC 3100

ATCGCCTGCCTTTGAAACTGAACGCTATGCACGAATGGCTCGAAATGATT

CCCTTAACTCCGTAGTATTGAGAGTGAGAGGAAAAGAAAAAAAGAGACAG 3200

AAAAGCTGACCATGGGAAAGAAGCATGATCAGTCGGGAATGGATCTGCGG

GTTGAGATAGATATGAGTTGCCTCGCAGATCCGGTGACAAGATAAGAGAA 3300

TTGGGAGATGTGATCAGCCACTGTAACTTCATCAAGCATCGACATTCAAC

GGTCGGGTCTGCGGGTTGAGATGCAAGTTGAGATGCCACGCAGACCCGAA 3400

CAGAGTGAGAGATGTGAGACTTTTGAACCACTGTGACTTCATCAAGCATC

AAAACACACTCCATGGTCAATCGGTTAGGGTGTGAGGGTTGATATGCCAG 3500

GTTCGATGCCACGCAGACCCGAACCGACTGAGAAATATGAAAAGTTGGAC

AGCCACTTCATCTTCATCAAGCGTAAAACCCCAATCAATGGTAAATCGAA 3600

AACGAATCTGCGGGCTGATGTGGAAATGAGACGAATGCCTCGCAGATTCG

AAGACACGTAAATCGAGATGAACAATCACTTTAACTTCATCAAAGCCTTA 3700

AATCACCCAATGGCCAGTCTATTCGGGTCTGCGGGTTGAGGTTCCTGTTG

AGATGCCACGCAGACTGCGAACATGCGATGCATTATAAGTTGGACGAGTG 3800

TAGACTGACCATTGATAACCGAGATAAACAATCACTTCAACTTCATCAAA

GCCTTAAATCACTCAATGGCCAGTCTGTTTGCGGTCTGCGGGCTGATACC 3900

CAAGTTGCGATGCCACGCAGACTGCAAACATTGATCGAGAGACGAGAAAA

ACAACGCACTTTAACTTCAACAAAAGCCTTTCAATCAGTCAATGGCCAGT 4000

FIG.6D

CTGTTCGCGGTCTGCGGGCTGATATGCGAGTTGAGGTGCCTCGCAGACCG

CGAACATGCGATGTAATTTCTTAGTTAGACGAGTGCCTGGCCATTGAGAA 4100

ACGAGAGAAACAACCACTTTAACTTCATGAAAGCCTTGAACTACTCAATG

ACCCGTCTGTTGGCGGTCTGCGGGCTGATATTCGAGTTGAGATGCCACGC 4200

AGACCGCCAACATGCGATGTATCATGTAAGTTAGATGAGTGACTGGCCAT

TGAGAAACGAGAGAAACAACCACACTTCATGAGAGCCTTAAATTATTCAA 4300

TGACCAGTCTGTTCACGGTCTGCGGGTTGGTATGCGAGTCGAGGTGCCTC

GCAGACCGCGAACATGCGATGTTTTCGATGGACGAGTGAAGCCTGACGAT 4400

CGAGAACTATCTCAGTTGGGTTGGCCATTCGGCTGGCCGTTGGGTTTAGT

ATTAGGATCGTCAGGTTTGTCCGATGGAACGTTCCGTTTGCGTGCGTTGG 4500

CGCGACGAGCCCTCTCCTCGGCGTGATTCTGAAATTCTGCAATCAGGGCA

GCCGCAGCACGGCGACGGGACGTCCTCCAGGAGCTGTGTTGAAGTTTCGG 4600

GGTGGCGGTCCAGAAGGGGGAGTTACATTAAAAGCCTCATAGATGTCTTT

GGGTGGTTCCGGGGGGCCCATCGCAAGATCTTCTGGAGTTGTGCGTCTGA 4700

TCATCTCTTGAGTGTAATTGCGACGCAGACCGAGCTTCAGGATTTTGGAA

GGGCTGGATCGCTCCTGCTGACTCTTTCCCTCAGCGGGCTTCGTCTCGGC 4800

AGTCTTCATTTCGGCGGGCTGATCTTCCATCTCAGAATGGGATCGCTTTC

TGGTCGCTGCACCCGCTCCTCCCTTCAAGGTCAGCTTGATGCGCAGCGTC 4900

TTGGGCGGCTCAGCTGGTGGAGTTGGTTCCGGCTCTGGCTCCCTCCGGCG

TCGCTTGGGCACTTGAGTAGTCTCTGAGGCTTCGCCGCGGCGCCGTTTGC 5000

FIG 6E

GAGTCGGCTCCTTGGTCTCTTTGGCCTCTTTCACTTCACCTGGACCGTCT

TTCGGGGCGGTTTCATCGTGCTGAGCGATCAAGGTTTGGATGTAGGCAGC 5100

CGGCATCATTCGATCAACGGCAATTCCTCTCTTGCGGGCCTCCTCCCGAG

CCTTGATTGTCGCCTTGACCTCGTCCACGTTTTCGAAGAAGAAAGGCATC 5200

TTGTTATCCTGAGGCAAGTTGCGCTCTCCCATGCGTGGGGATATCCGAAG

ATGCGGTCCTTCTCGAACTGTTCATGAGACTTCAGACGAATTGGAGGCTG 5300

GGGGAGCAATTTGTCTCCGTAGGTGTTGTTAGGGCGGAACCAAGAATAGC

CTTCGCCTACAACGACAAGCTCTTCGCCAAATTTATTTTTTTGGCCTGTA 5400

AAAACGAACCCATCCTCGTCAGTCCACCGGTGCGTCTCGGACGTAGAGAT

TGGCTTACTTATTCCCTCAACGCCGATCTCTGCCTGGGGCTGCGCTTCGG 5500

ATGCGGCCTCGGTCACGGCTCCGCCTCGGACTGCACCGCTGGAGTTTCGG

TCTTCTTCTCCTGCTTCTCCAGGTACTCCTTGCGTAACTCTTCGATCAGC 5600

CTCGGCTTCCGATGACTGCTCAAATTCTGGAGCAACAGCTGCCGCGGCCA

GGTCAAGCAGGCGGTTTGCTAAAACTGCCCATTTTCCATCGACACCTGCC 5700

TCCGACGCCTGTGCAAAACCAGCTGTTTTCGCATTGGCCTGTTTGTTGGC

ACGCGTCTTCTTGACTGCTGCCTTGCCCTTTACTTCCTTGAGAGCAGACT 5800

CTGGCTTAGATGATGGTGCACGGTTTCTGCGGAAGCGCCGCTCAGATTCC

AAAGATTCCATAGCTTTAATGGTAGGCTTTCTGGTTCTTCCAGAAGTGCG 5900

CGCAGCTGACGTAGTGGTTGAGTAGCTGGCAGTTGGGGATCCTGGGCCCT

CATTGGAACCATCAAGACCAAATTTGTTTCCATACATATCAGCATGGTAT 6000

FIG.6F

TCAAAAGGAAAACTTTCGCCGTACGGAGTACTGCGTTCGATTCCGGGTGT

ATCCAAGTCGTATCCAGACATGGTGTCGAATTCAGCCTTGCTGTCAAGAG 6100

CAGGGGTACTTTCAATGCTGTCAGCAACCACGCGGCCAAAGGGCGTCTTC

GGGAAAGAAGGTGTTTCAAGAGAAGCGTCATCCACGGCCTGGCTTGCGGC 6200

GTTGATTGCAGACTTTCGAGTAGATCGCTGAGGTCGCGAACTGGTTCGAG

TAGCAACCTGTGAATTGGCAGCCTTGTGACTGCTTCGATTCACTGCAGAG 6300

ACGGAGTAGACTGCACTGATTTGGAATTCTGAGTCGCAGCCATTCTGGAT

TTGCGTTCGGCGCGACGAGATCTCGCAGTCGTGGTACGAGGAGTAGAGCG 6400

AGGCTGCGTAGCAGTGTTGCAAGCTTGGTGCTAGCCTCCTGGGCTTCAGC

AGCTTCAGCAGTGGTGGCAGACGCAGCAGAATTAGCGGAGCTTTATCGGC 6500

TTTGCCGCTCTGAGCGTTGGGAGTAGAAGTGAGAGAAGAGGTAGAGTCCA

CGGAAGAAGTCTTCTCGCTGTTCTCAAAGCCGTTCAGCTTTGCTGGCATA 6600

GACTTACGCGTCTTGCGGCTGTTGGAAGCGGAAGAGTTCATGGCGGGAGA

GGAGACGTTAGAAGTAGACATGGTGGGGTTTGTTGACGGGTTTTGAGTAA 6700

CAAGAGACTTGCGTCGATCTTTGAGTGTTCTTGACAGAAAGTTATGCAAC

GTCGAC 6756
SalI

FIG.6G

PHYTASE LOCUS

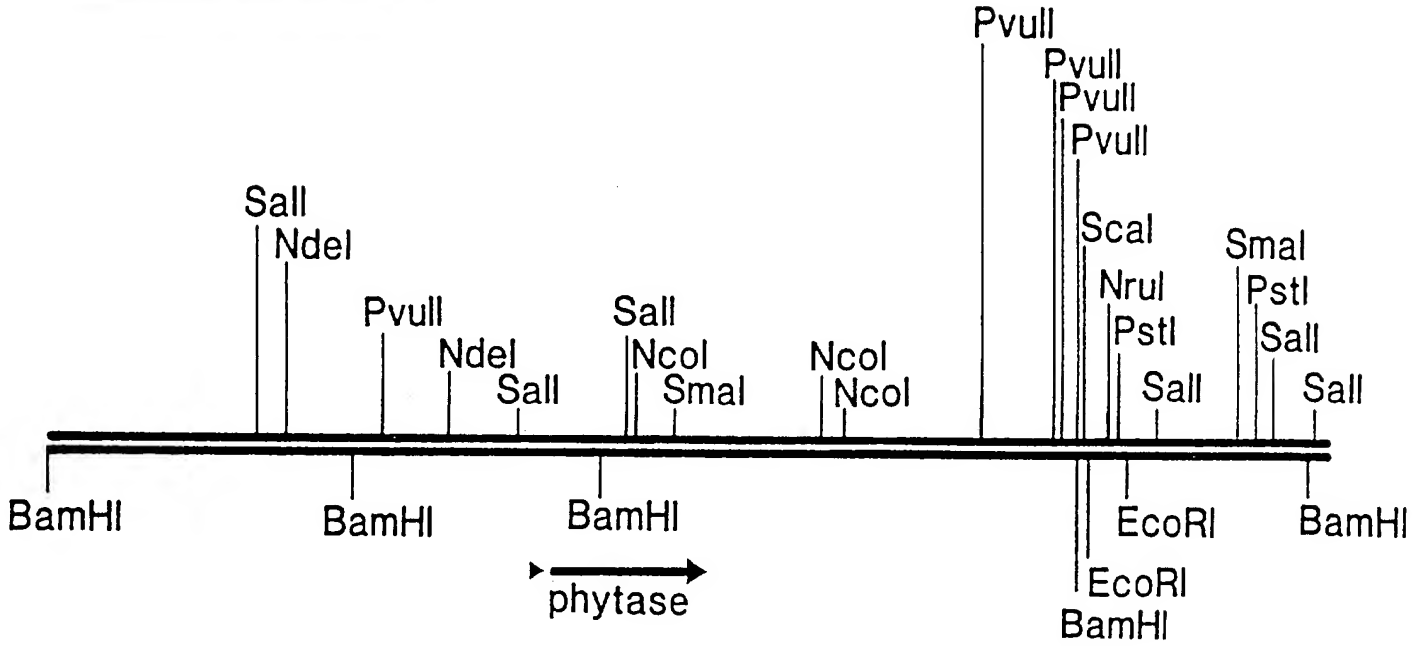

FIG.7

```
ATGGGCGTCTCTGCTGTTCTACTTCCTTTGTATCTCCTGTCTGGAGTCAC
 M  G  V  S  A  V  L  L  P  L  Y  L  L  S  G  V  T
-23      -20              '             -10

CTCCGGACTGGCAGTCCCCGCCTCGAGAAATCAATCCAGTTGCGATACGG      100
  S  G  L  A  V  P  A  S  R  N  Q  S  S  C  D  T
     '          -1 +1          '              10

TCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGGTCAA
V  D  Q  G  Y  Q  C  F  S  E  T  S  H  L  W  G  Q
          '              20              '

TACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCATCTCCCCTGAGGT      200
 Y  A  P  F  F  S  L  A  N  E  S  V  I  S  P  E  V
      30              '              40

GCCCGCCGGATGCAGAGTCACTTTCGCTCAGGTCCTCTCCCGTCATGGAG
  P  A  G  C  R  V  T  F  A  Q  V  L  S  R  H  G
  '              50              '              60

CGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCGCTCTCATTGAG      300
A  R  Y  P  T  D  S  K  G  K  K  Y  S  A  L  I  E
          '              70              '

GAGATCCAGCAGAACGCGACCACCTTTGACGGAAAATATGCCTTCCTGAA
 E  I  Q  Q  N  A  T  T  F  D  G  K  Y  A  F  L  K
      80              '              90

GACATACAACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAAC      400
  T  Y  N  Y  S  L  G  A  D  D  L  T  P  F  G  E
  '              100             '              110

AGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAGCGGTACGAATCGCTC
Q  E  L  V  N  S  G  I  K  F  Y  Q  R  Y  E  S  L
          '              120             '

ACAAGGAACATCGTTCCATTCATCCGATCCTCTGGCTCCAGCCGCGTGAT      500
 T  R  N  I  V  P  F  I  R  S  S  G  S  S  R  V  I
     130              '              140

CGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCACCAAGCTGAAGG
  A  S  G  K  K  F  I  E  G  F  Q  S  T  K  L  K
  '              150             '              160

ATCCTCGTGCCCAGCCCGGCCAATCGTCGCCCAAGATCGACGTGGTCATT      600
D  P  R  A  Q  P  G  Q  S  S  P  K  I  D  V  V  I
          '              170             '

TCCGAGGCCAGCTCATCCAACAACACTCTCGACCCAGGCACCTGCACTGT
 S  E  A  S  S  S  N  N  T  L  D  P  G  T  C  T  V
     180              '              190

CTTCGAAGACAGCGAATTGGCCGATACCGTCGAAGCCAATTTCACCGCCA      700
  F  E  D  S  E  L  A  D  T  V  E  A  N  F  T  A
  '              200             '              210
```

FIG.8A

```
CGTTCGTCCCCTCCATTCGTCAACGTCTGGAGAACGACCTGTCCGGTGTG
T  F  V  P  S  I  R  Q  R  L  E  N  D  L  S  G  V
         '           220                    '

ACTCTCACAGACACAGAAGTGACCTACCTCATGGACATGTGCTCCTTCGA      800
 T  L  T  D  T  E  V  T  Y  L  M  D  M  C  S  F  D
    230                 '           240

CACCATCTCCACCAGCACCGTCGACACCAAGCTGTCCCCCTTCTGTGACC
  T  I  S  T  S  T  V  D  T  K  L  S  P  F  C  D
  '           250                 '           260

TGTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCTTGAAA      900
L  F  T  H  D  E  W  I  N  Y  D  Y  L  Q  S  L  K
         '           270                    '

AAGTATTACGGCCATGGTGCAGGTAACCCGCTCGGCCCGACCCAGGGCGT
 K  Y  Y  G  H  G  A  G  N  P  L  G  P  T  Q  G  V
    280                 '           290

CGGCTACGCTAACGAGCTCATCGCCCGTCTGACCCACTCGCCTGTCCACG     1000
  G  Y  A  N  E  L  I  A  R  L  T  H  S  P  V  H
  '           300                 '           310

ATGACACCAGTTCCAACCACACTTTGGACTCGAGCCCGGCTACCTTTCCG
D  D  T  S  S  N  H  T  L  D  S  S  P  A  T  F  P
         '           320                    '

CTCAACTCTACTCTCTACGCGGACTTTTCGCATGACAACGGCATCATCTC     1100
 L  N  S  T  L  Y  A  D  F  S  H  D  N  G  I  I  S
    330                 '           340

CATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAGCCGCTATCTACCA
  I  L  F  A  L  G  L  Y  N  G  T  K  P  L  S  T
  '           350                 '           360

CGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGTCTGCTTGGACG     1200
T  T  V  E  N  I  T  Q  T  D  G  F  S  S  A  W  T
         '           370                    '

GTTCCGTTTGCTTCGCGTTTGTACGTCGAGATGATGCAGTGTCAGGCGGA
 V  P  F  A  S  R  L  Y  V  E  M  M  Q  C  Q  A  E
    380                 '           390

GCAGGAGCCGCTGGTCCGTGTCTTGGTTAATGATCGCGTTGTCCCGCTGC     1300
  Q  E  P  L  V  R  V  L  V  N  D  R  V  V  P  L
  '           400                 '           410

ATGGGTGTCCGGTTGATGCTTTGGGGAGATGTACCCGGGATAGCTTTGTG
H  G  C  P  V  D  A  L  G  R  C  T  R  D  S  F  V
         '           420                    '

AGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCGGAGTGTTTTGC     1400
 R  G  L  S  F  A  R  S  G  G  D  W  A  E  C  F  A
    430                 '           440

TTAG                                                   1404
```

FIG.8B

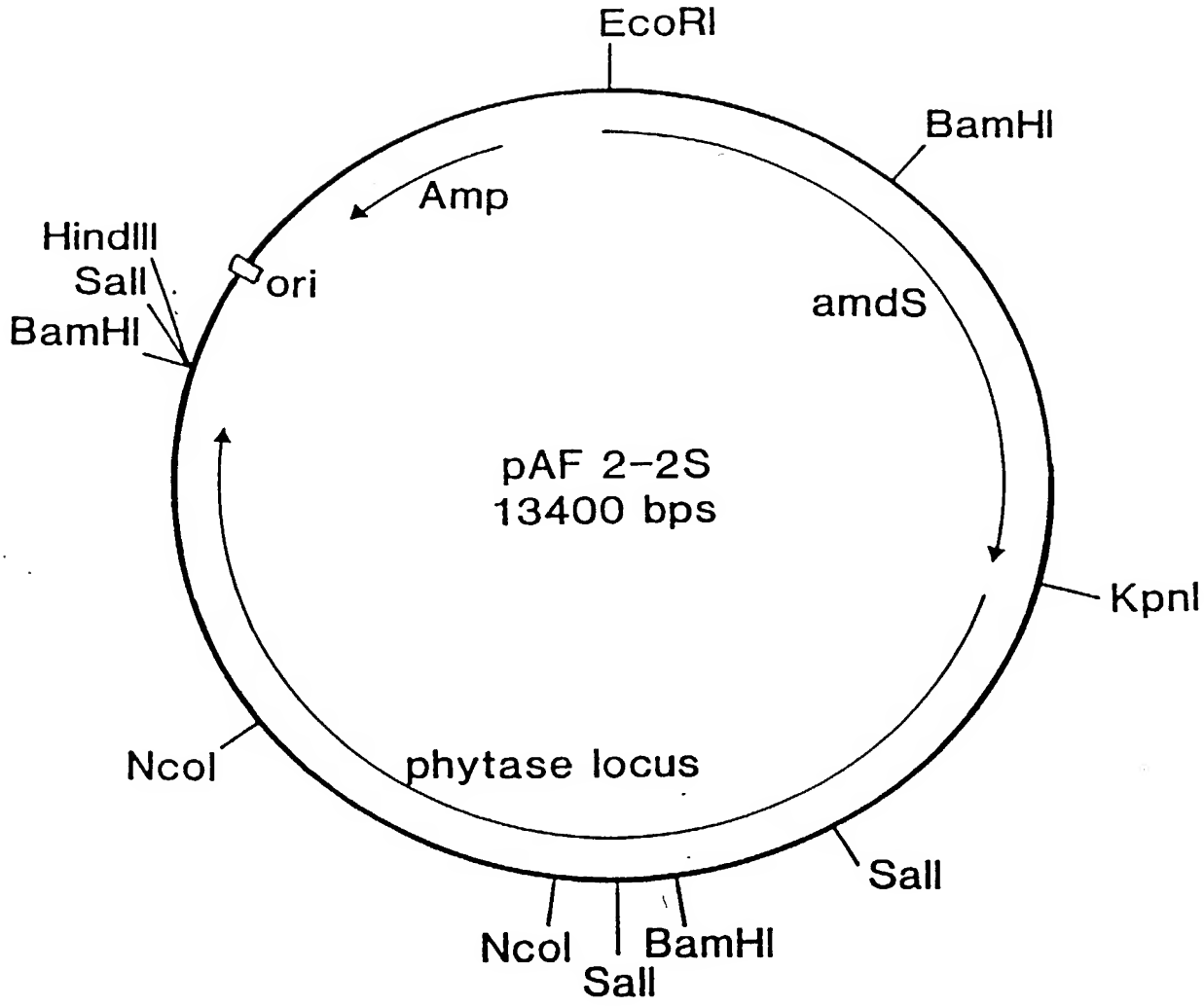

FIG.9

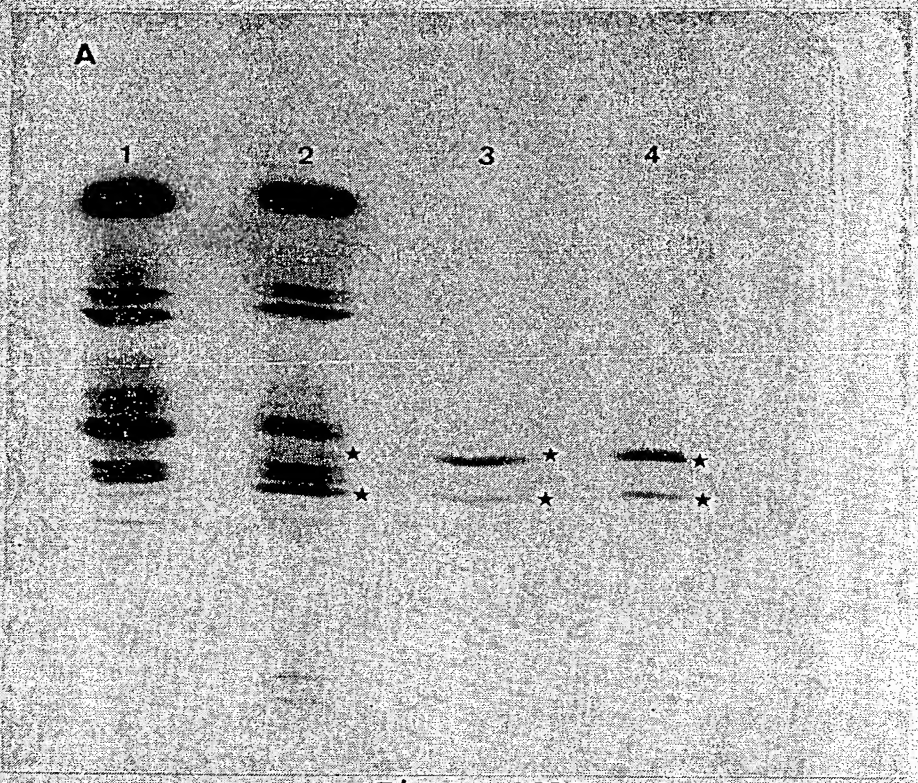

Figure 10A

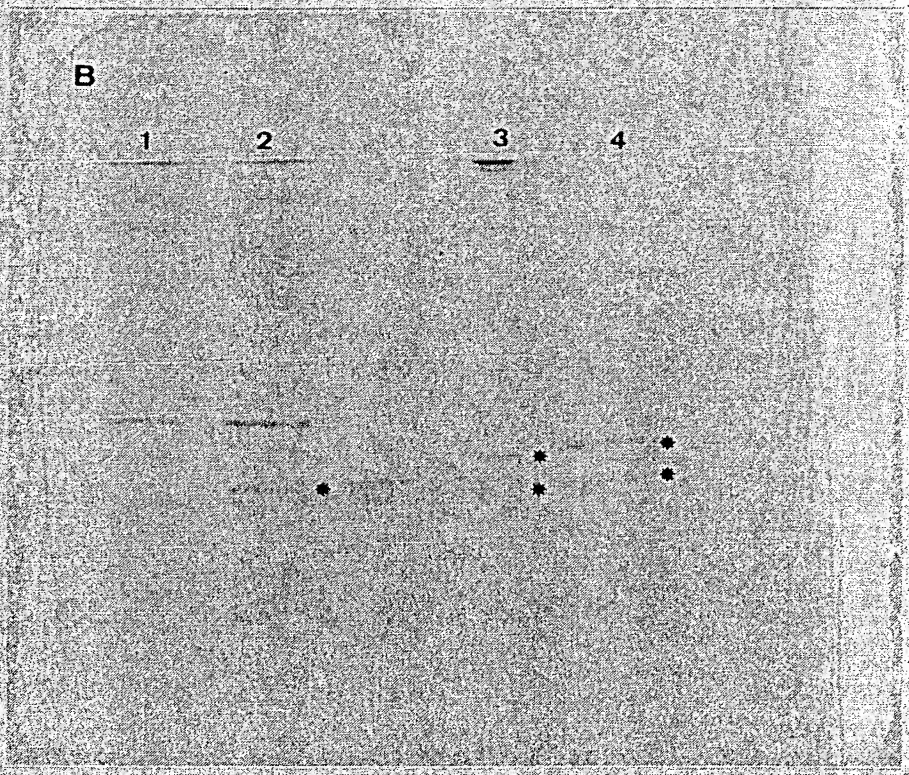

Figure 10B

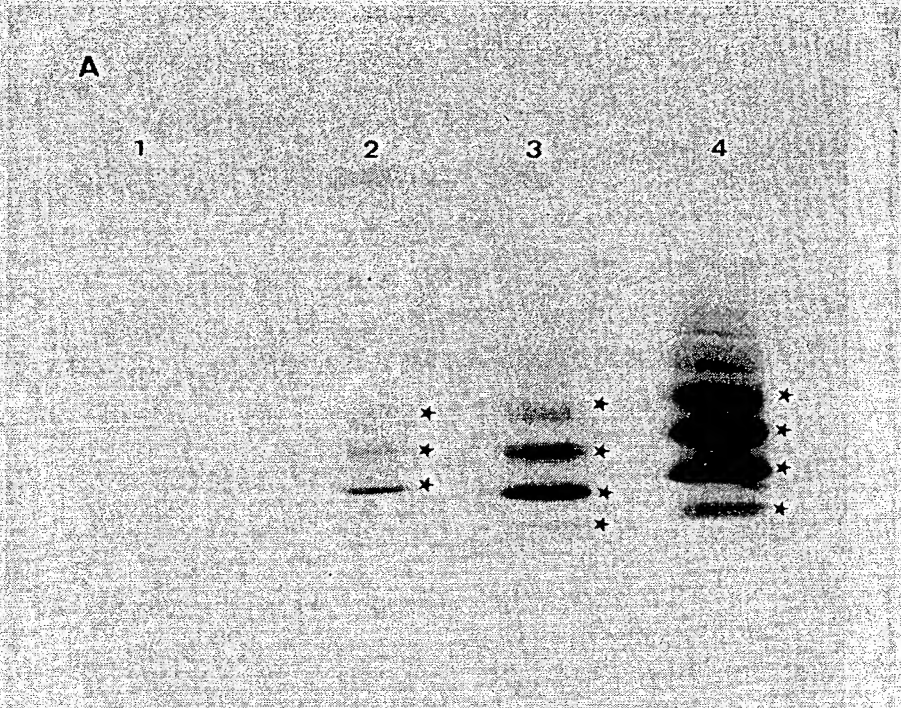

Figure 11A

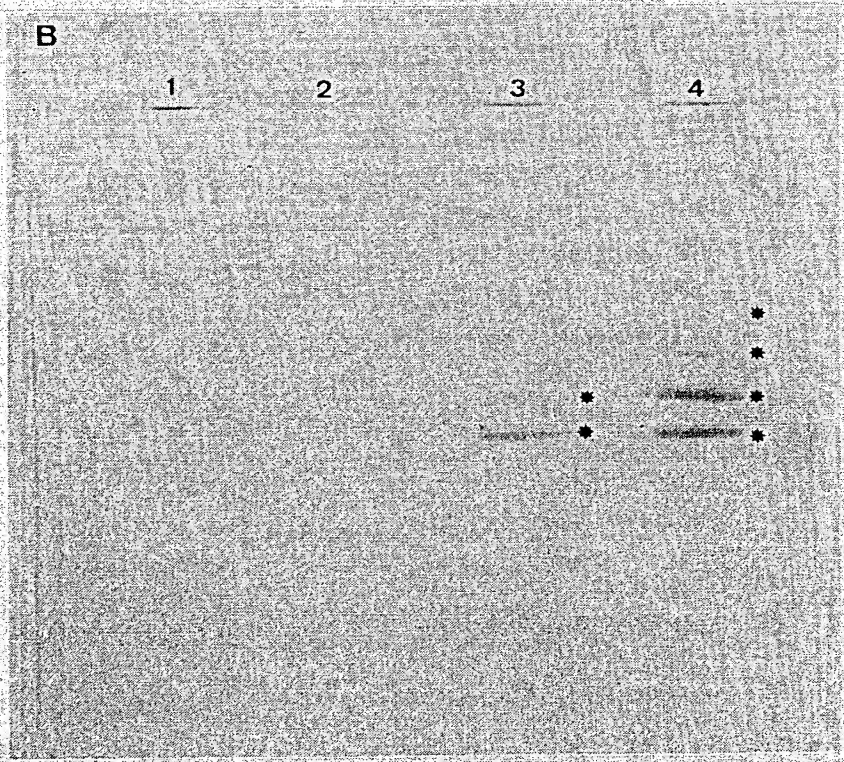

Figure 11B

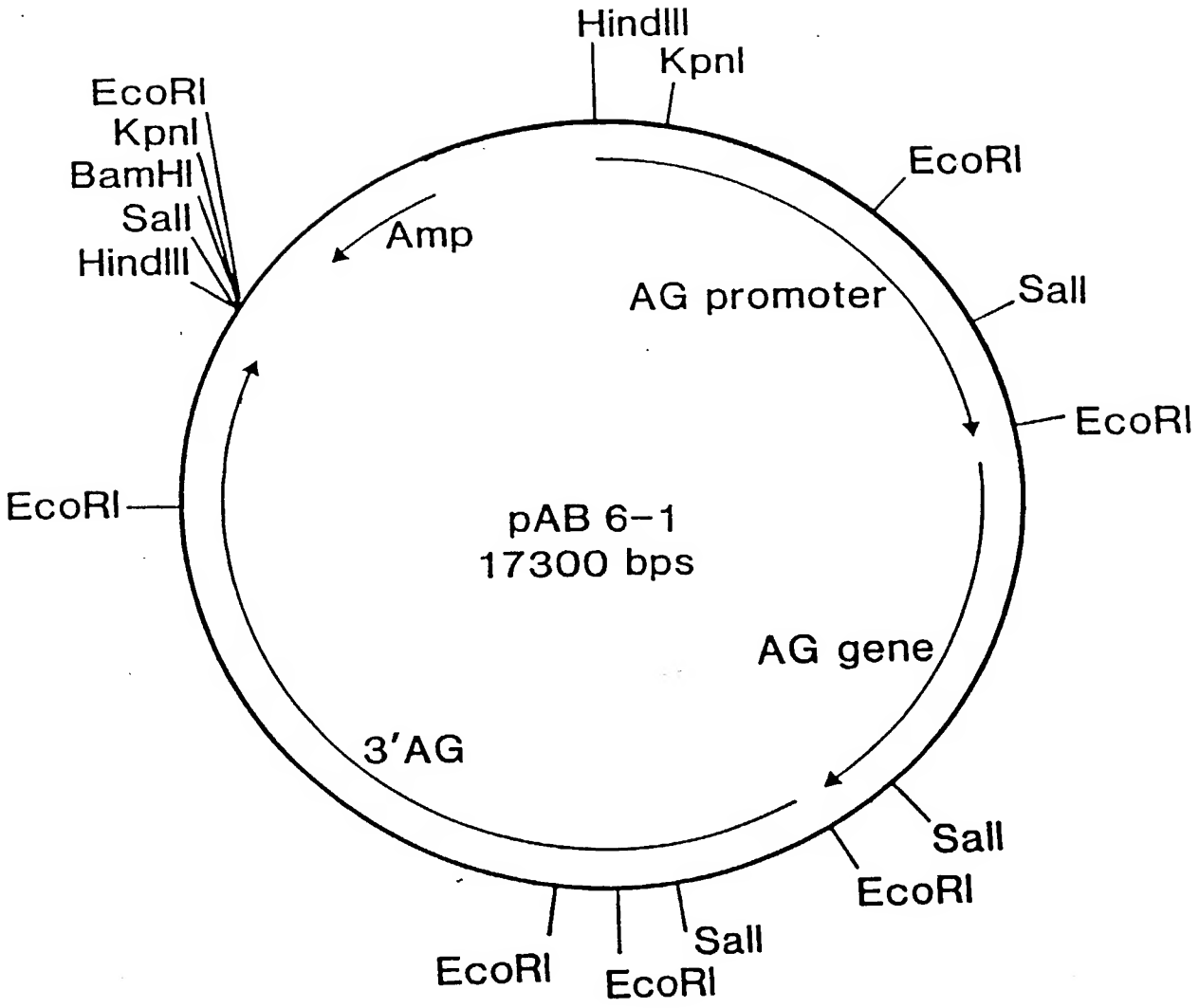

FIG. 12

AG/PHYTASE GENE FUSIONS BY PCR

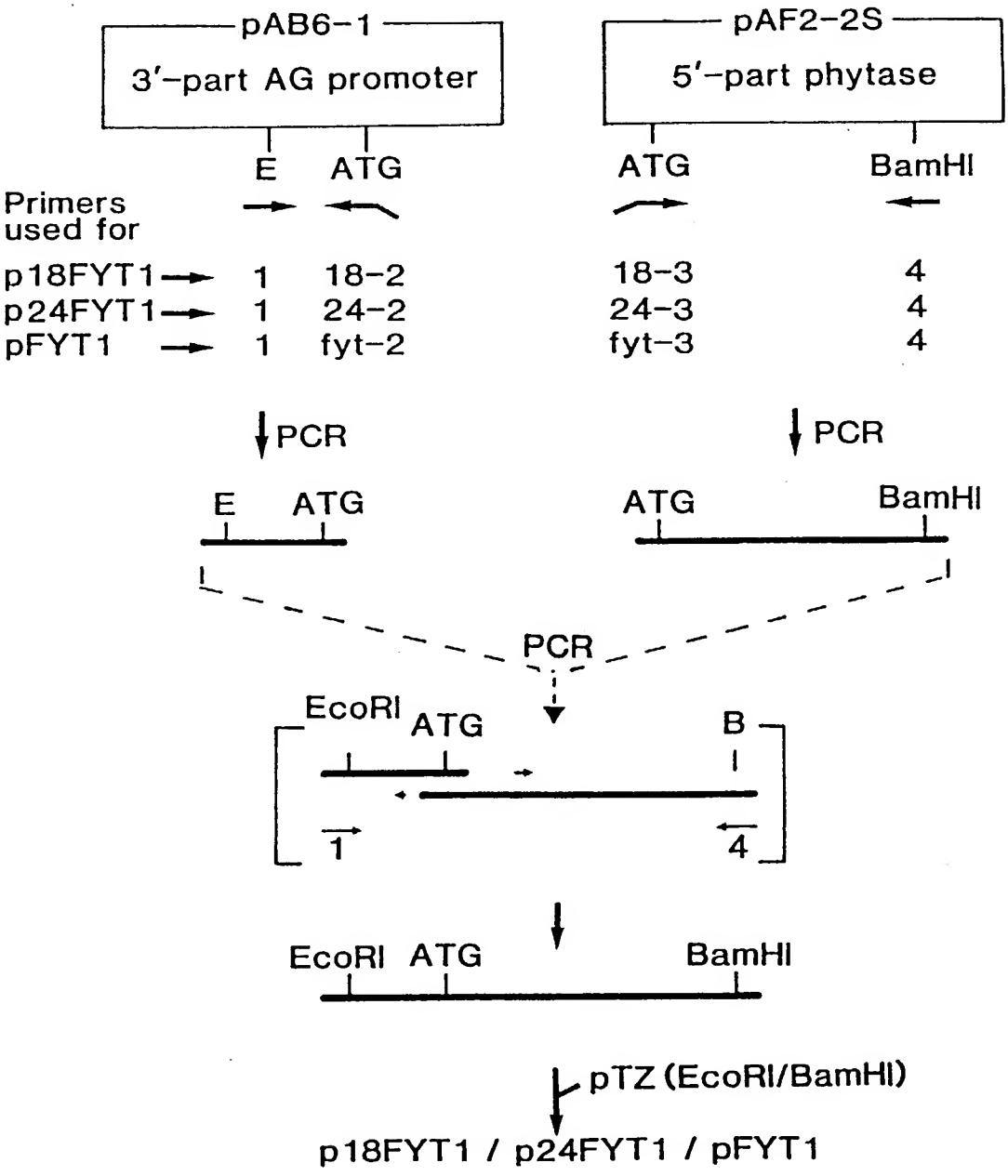

FIG. 13

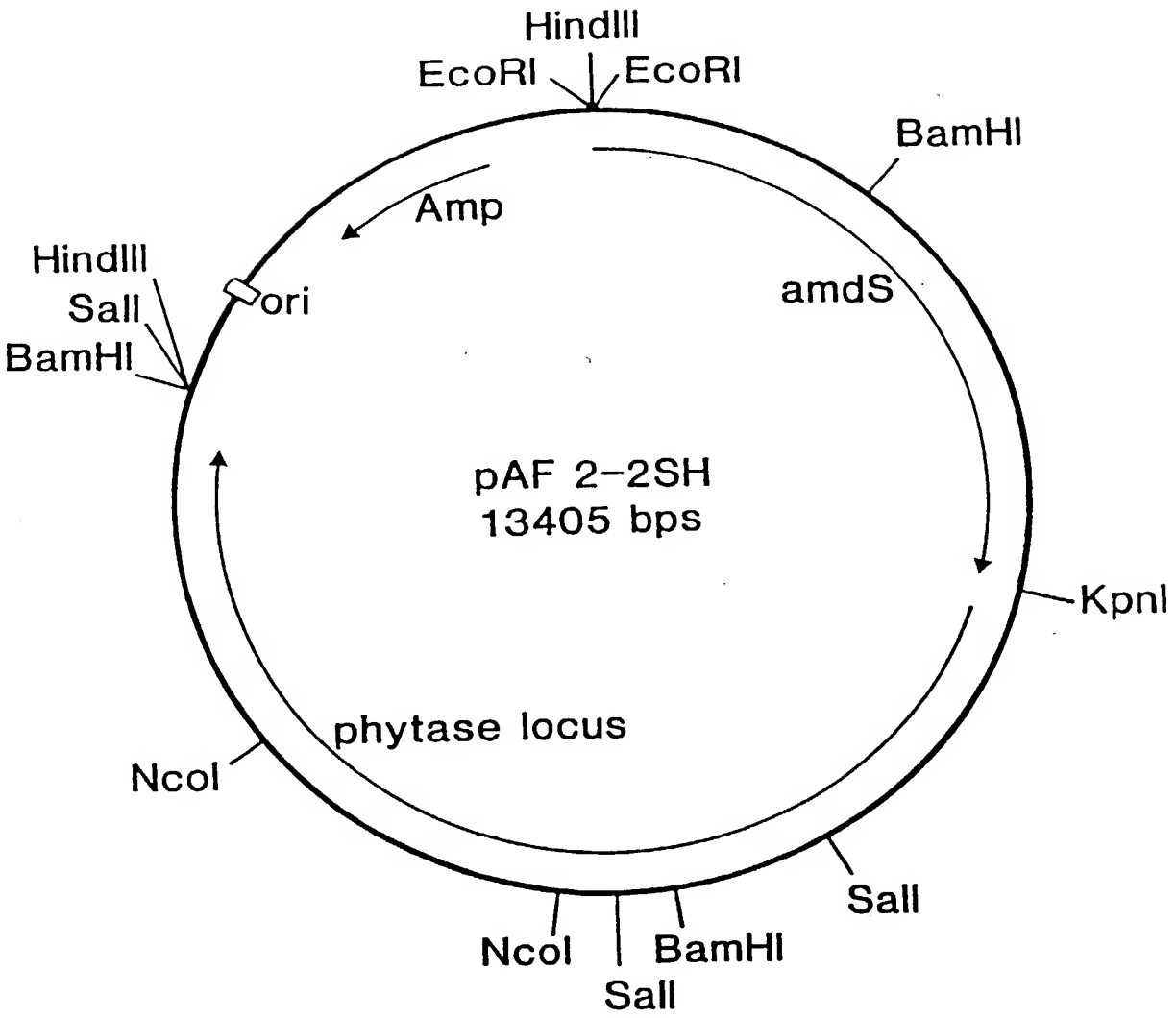

FIG. 14

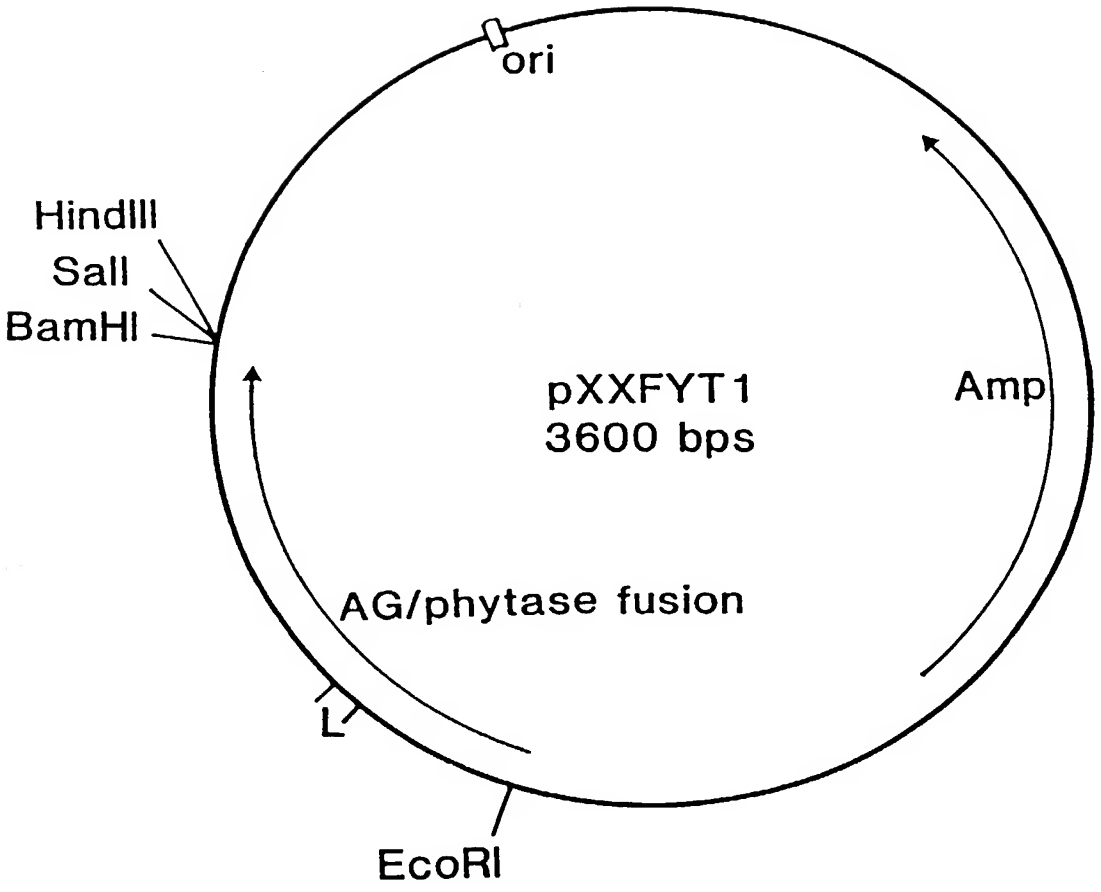

FIG. 15A

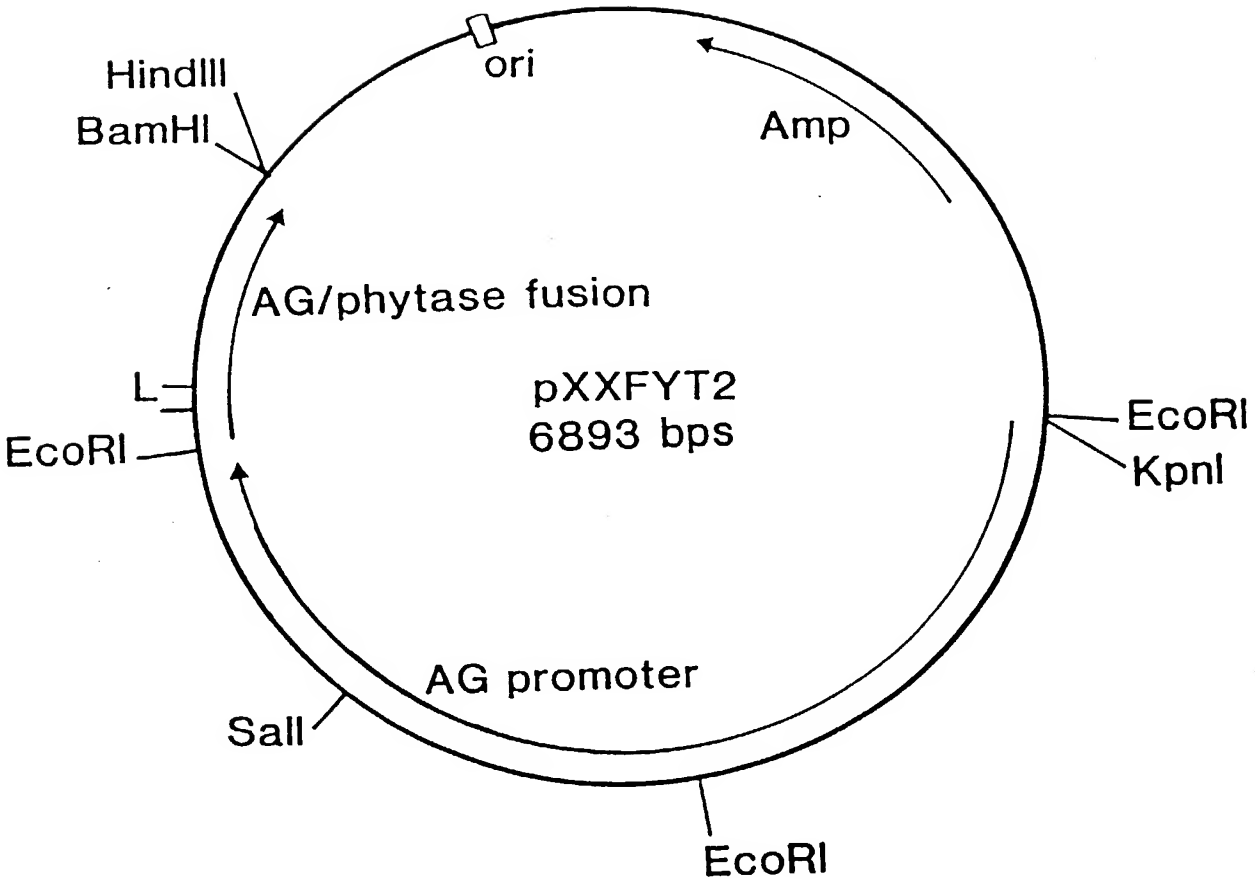

FIG. 15B

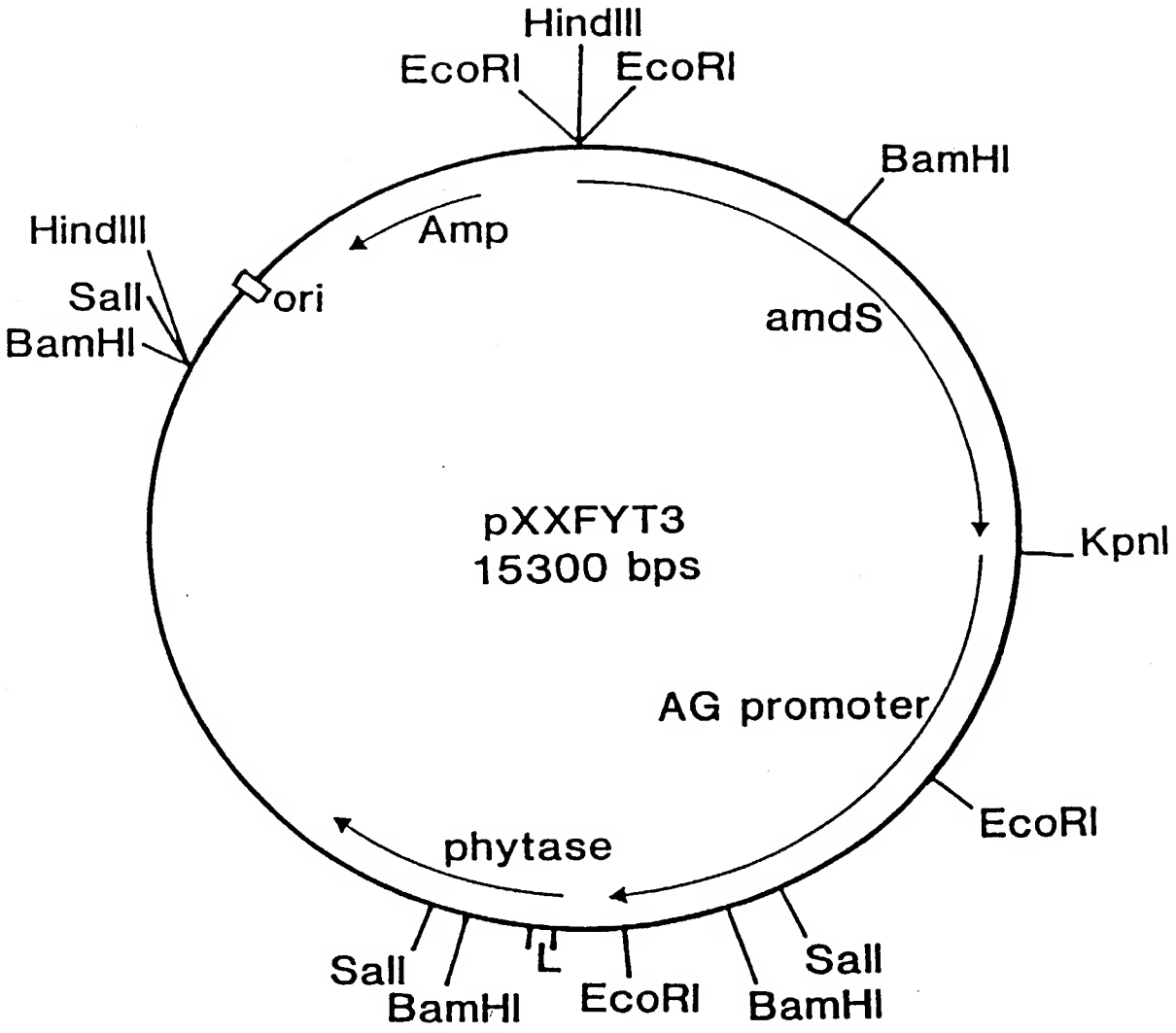

FIG. 15C

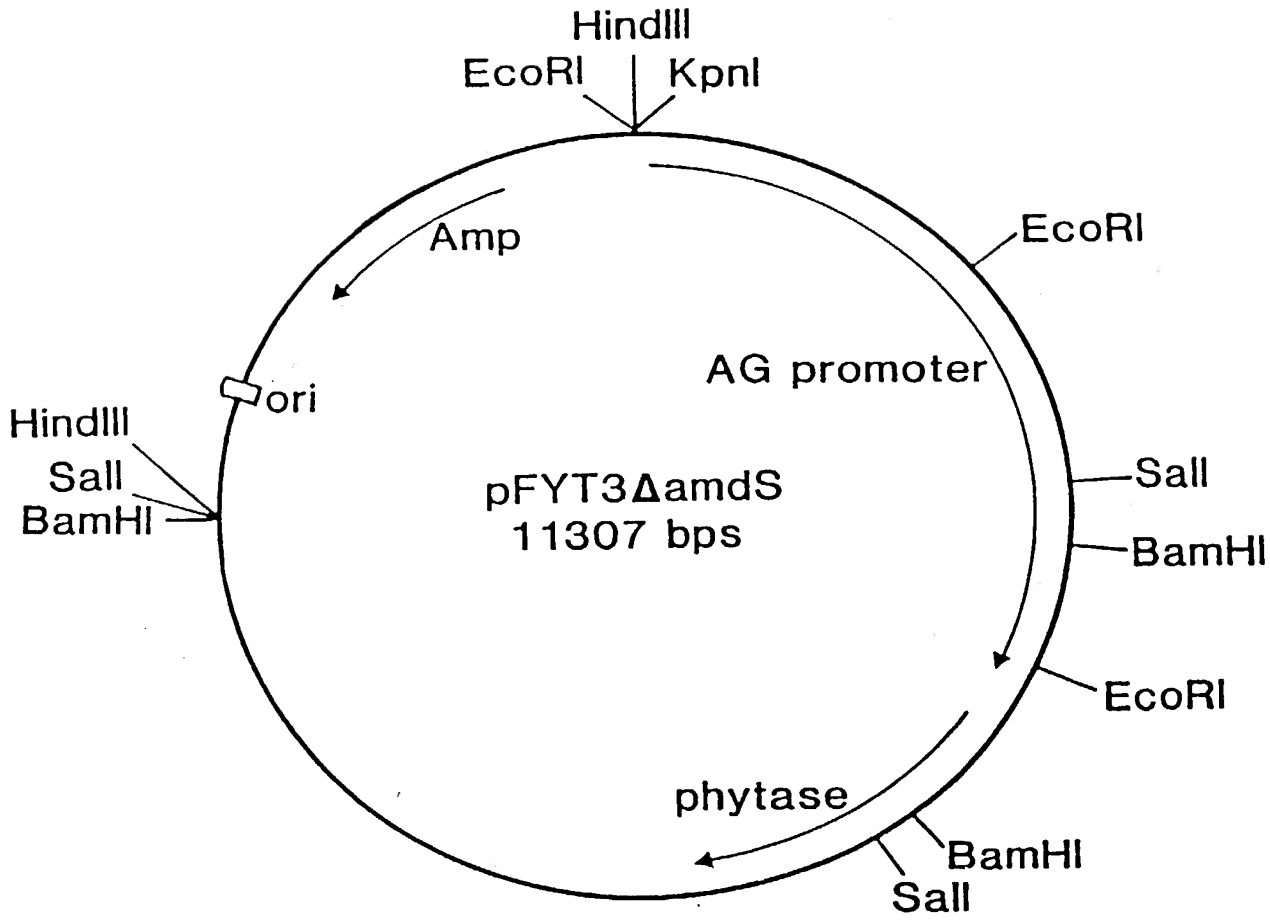

FIG. 16

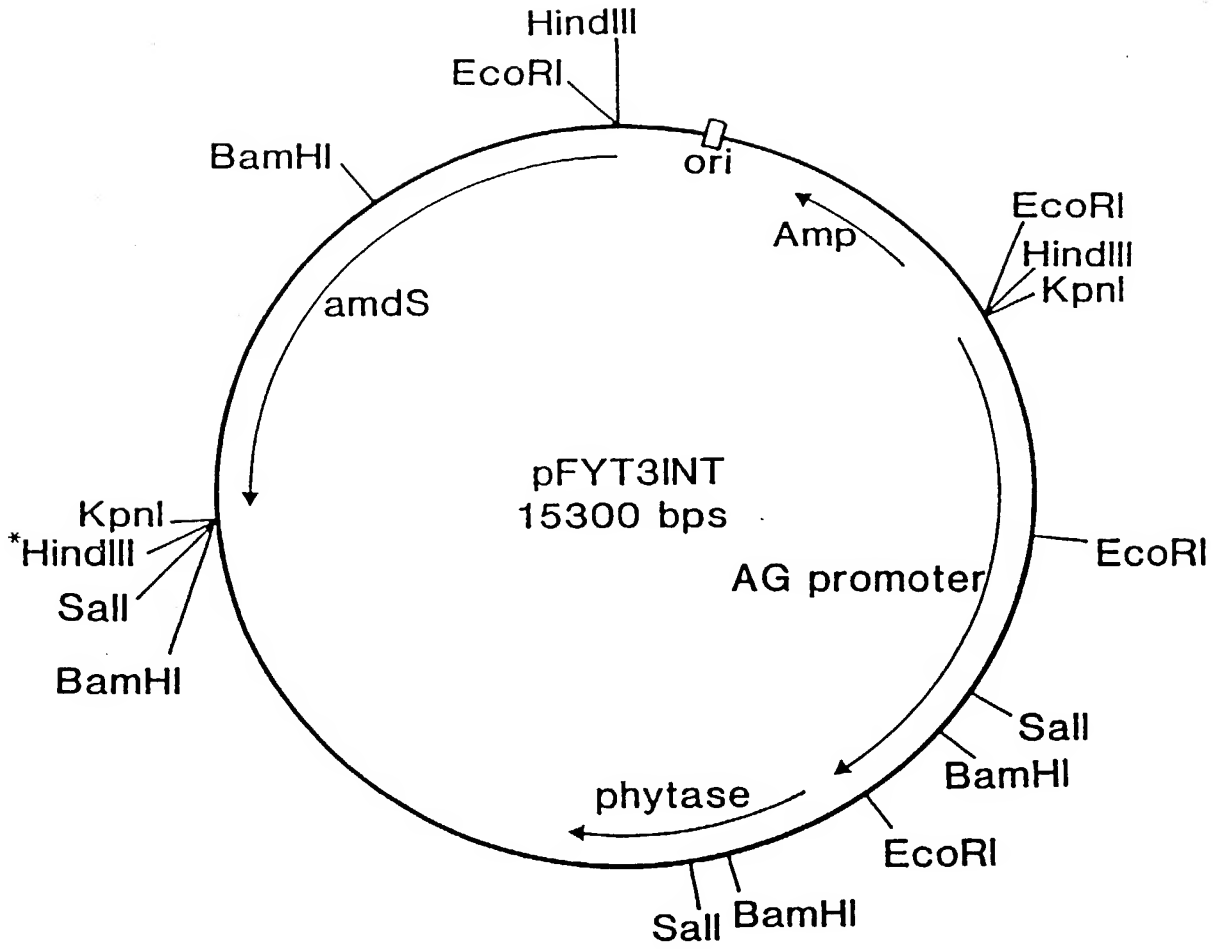

FIG. 17

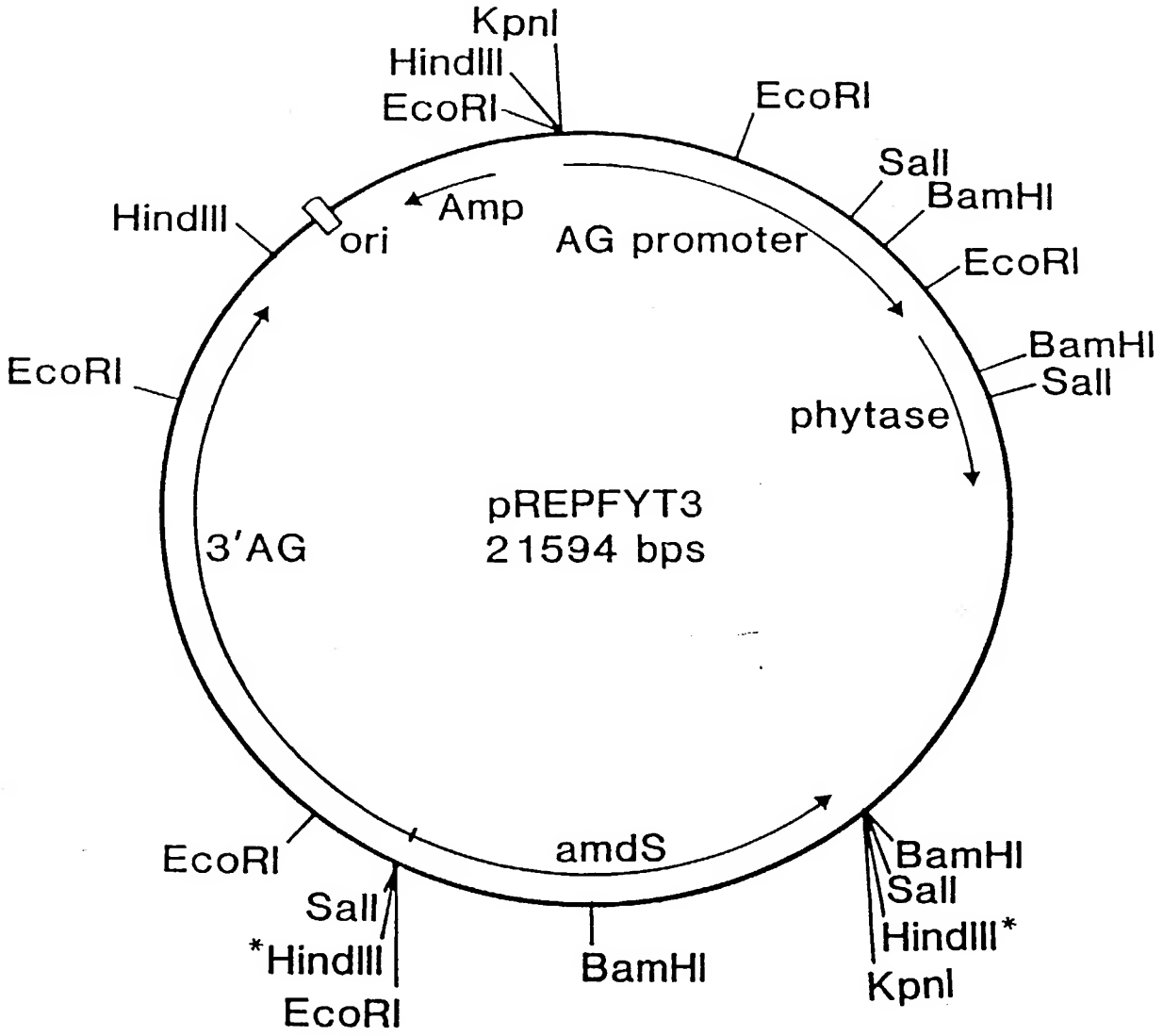

FIG. 18

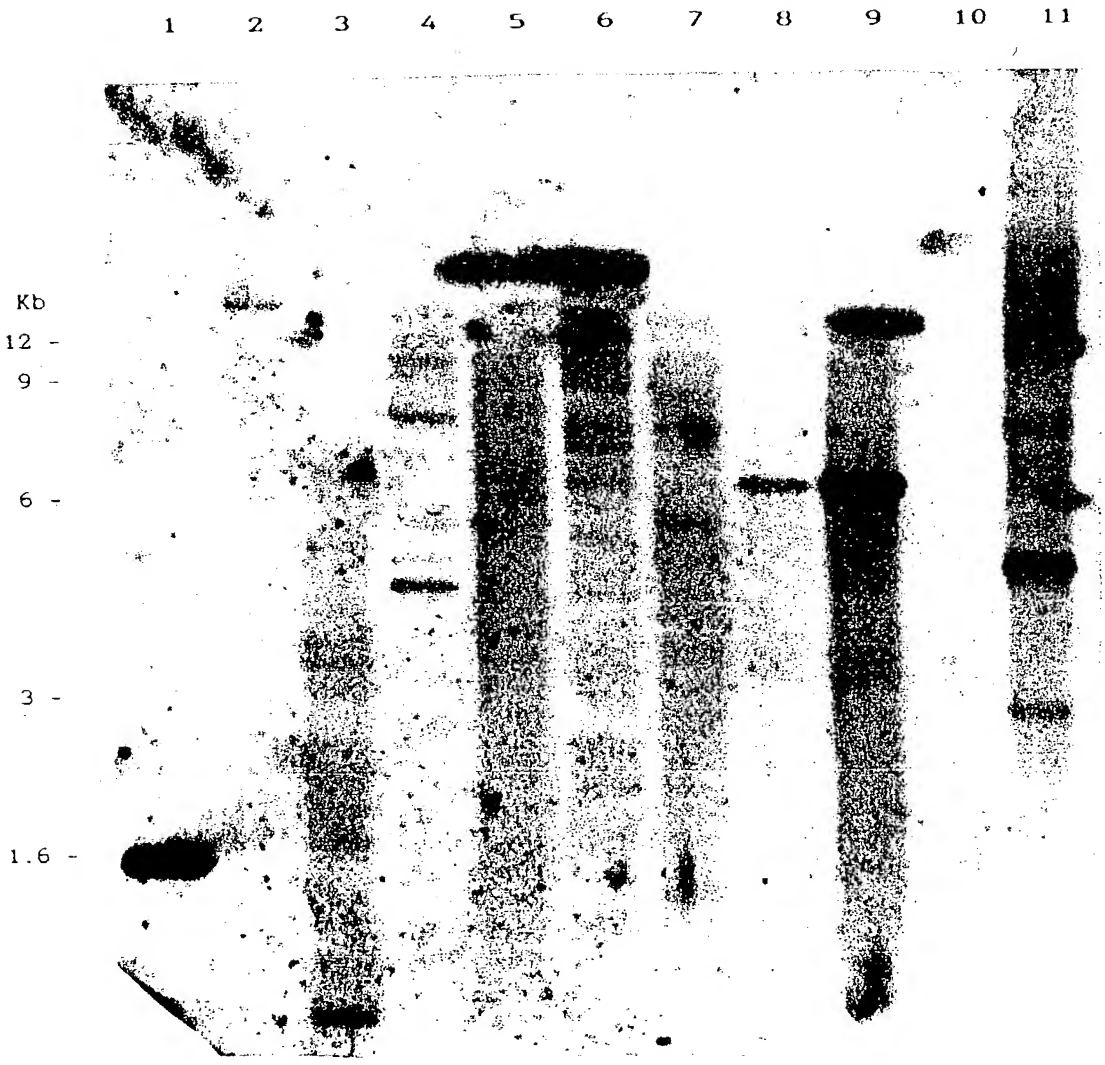

Figure 19A

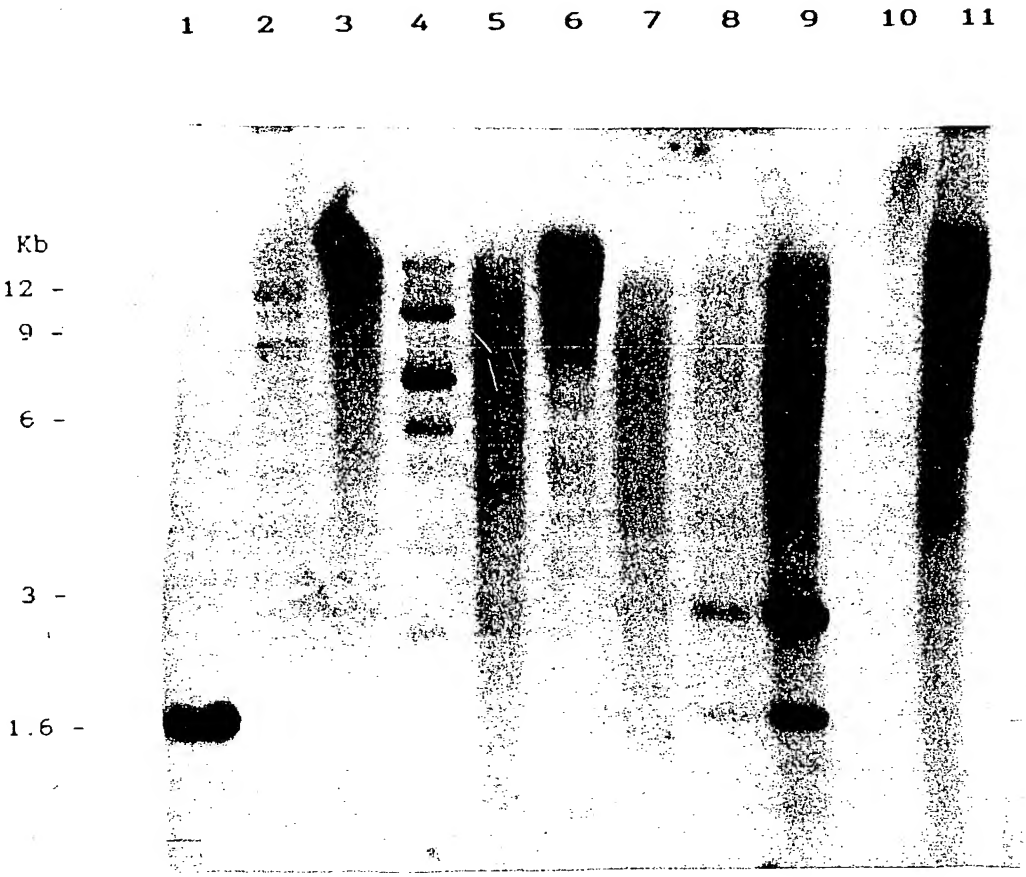

Figure 19B